SOME ON ADAPTIVE CONTROL OF A WASTEWATER BIODEGRADATION PROCESS

Dan SELIŞTEANU, Emil PETRE

Department of Automatic Control, University of Craiova A.I. Cuza Str. No. 13, RO- 200585, Craiova, Romania, E-mail: dansel@automation.ucv.ro, epetre@automation.ucv.ro

Abstract: In this paper some nonlinear adaptive control strategies are developed for a depollution biotechnological process. This bioprocess is in fact a biomethanation process - wastewater biodegradation with production of methane gas that takes place inside a Continuously Stirred Tank Bioreactor. Dynamical feedback controllers, nominally achieving output stabilization via exact linearization, are obtained by means of adaptive control ideas. The adaptive controllers are obtainable via standard, direct, overparametrized adaptive control techniques. A high gain estimation strategy is also used for identification of unknown kinetics of the bioprocess. Computer simulations are included in order to evaluate the performances of the adaptive controlled bioprocess.

Keywords: Water pollution, Waste treatment, Biotechnology, Nonlinear models, Estimators, Adaptive control

1. INTRODUCTION

In the modern industry, the development of advanced control strategies for biotechnological processes is hampered by major difficulties [1], [2]. These processes are strongly nonlinear and nonstationary and furthermore the process parameters are highly uncertain. Another difficulty lies in the absence, in most cases, of cheap and reliable instrumentation. In order to overcome these difficulties several strategies were developed, such as adaptive approach [1], vibrational control, predictive control, sliding mode control, fuzzy and neural strategies and so on. Today, the use of modern control for wastewater treatment plants is low. A main reason is the lack of quality of the data, and the fact that more sophisticated control strategies must be based on a model of the dynamics of the process [8]. When biotechnology strategies are used in wastewater treatment, the abovementioned properties of the bioprocesses require enhanced modelling an effort, modern estimation

strategies for the bioprocess kinetics and advanced control strategies. The non-linearity of the bioprocesses and the uncertainty of kinetics impose the adaptive control strategy as a suitable approach.

In industry, the bioprocesses take place in biological reactors, also called bioreactors. The bioreactors can operate in three modes: the continuous mode, the fed-batch mode and the batch mode [1], [2]. For example, a Fed-Batch Bioreactor (FBB) initially contains a small amount of substrates and microorganisms and is progressively filled with the influent substrates. When the FBB is full the content is harvested. By contrast, in a Continuously Stirred Tank Bioreactor (CSTB) the substrates are fed to the bioreactor continuously and an effluent stream is continuously withdrawn such that the culture volume is constant.

The difficulties encountered in the measurement of the state variables of the bioprocesses (substrates, biomass, product concentrations and so on) impose the use of so-called "software sensors". A software sensor is a combination between a hardware sensor and a software estimator. These software sensors are used not only for the estimation of the concentrations the state variables - but also for the estimation of the kinetic parameters. Very important is the estimation of kinetic rates inside a bioreactor the estimates of these rates are used for advanced control strategies. The interest for development of software sensors for bioreactors is proved by the big number of publications and applications in this area [1], [3], [8]. The first approach from historically point of view is based on Kalman filter which leads to complex nonlinear algorithms. Well-known is the Bastin and Dochain approach based on the adaptive systems theory [1]. Another possibility is to design an estimator using a high gain approach (see [3], [4], [10], [11]). The gain expression of these simple observers involves a single tuning parameter whatever the number of components and reactions.

In this paper, adaptive linearizing control laws are proposed for a biomethanation depollution process that takes place inside a CSTB. Overparametrization and the availability of the dynamical controller state variables are the key issues that allow application of the direct adaptive control techniques. Major contributions in this field were given by Sastry and Isidori [9], Narendra *et al.* [7]. The reaction kinetics of the biomethanation process (more precisely, the specific growth rates) are estimated using a high-gain observer.

This work is organized as follows. In Section 2, the model of a wastewater biodegradation process inside a Continuous Stirred Tank Bioreactor (CSTB) is presented. Section 3 deals with the design of an exactly linearizing control law for the biodegradation process, using a reduced order input-output model of the bioprocess. Next, an adaptation law obtained by means of a Lyapunov technique is applied for an unknown parameter of the process; subsequently an adaptive controller is obtained combining the exactly linearizing control law and the adaptation law. In Section 4, the exactly linearizing controller, the adaptation law and finally the adaptive controller are achieved using the complete model of the bioprocess. Furthermore, the unknown reaction kinetics of the bioprocess are on-line estimated using a high gain observer. In order to analyse the performances of the controllers, computer

simulations are provided. Section 5 collects concluding remarks.

2. THE BIODEGRADATION PROCESS MODEL

A highly important biotechnological process is the wastewater biodegradation with production of methane gas [1], [11]. This anaerobic degradation process is a commonly method of wastewater treatment, which consists in four metabolic phases: two phases for acid production and two phases for methanation. In the first phase, the glucose from the wastewater is decomposed in fat volatile acids (acetates, propionic acid), hydrogen and inorganic carbon under action of the acidogenic bacteria. In the second phase, the ionised hydrogen decomposes the propionic acid CH₃CH₂COOH in acetates, H₂ and carbon dioxide CO₂. In the first methanogenic phase, the acetate is transformed into methane and CO₂, and finally in the second methanogenic phase, the methane gas CH₄ is obtained from H₂ and CO₂.

The reaction scheme of this complex bioprocess involves 4 reactions and 10 components [1]. From the reaction scheme we can obtain the dynamical model of this bioprocess that takes place inside a CSTB, considering the mass balance of the components (see [1], [11]). The obtained dynamic model is very complex and the design of useful control strategies is hampered because of this large dimension (ten) of the model. So it is necessary to reduce the order of this model, taking into consideration some particular aspects of the process and using the singular perturbation theory [6]. A simplified reaction scheme and the corresponding model can be derived for this bioprocess (see [11]):

$$\begin{cases} S_{1} \xrightarrow{\phi_{1}} X_{1} + S_{2} \\ S_{2} \xrightarrow{\phi_{2}} X_{2} + P \end{cases}$$

$$\frac{d}{dt} \begin{bmatrix} X_{1} \\ S_{1} \\ X_{2} \\ S_{2} \\ P \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ -k_{1} & 0 \\ 0 & 1 \\ k_{2} & -k_{3} \\ 0 & k_{4} \end{bmatrix} \begin{bmatrix} \phi_{1} \\ \phi_{2} \end{bmatrix} - D \begin{bmatrix} X_{1} \\ S_{1} \\ X_{2} \\ S_{2} \\ P \end{bmatrix} + \begin{bmatrix} 0 \\ DS_{in} \\ 0 \\ 0 \\ -Q \end{bmatrix}$$

$$(2)$$

In the reaction scheme (1), S_{i} , i=1,2 are substrates: S_1 represents the glucose, S_2 the acetate, X_1 is the acidogenic bacteria, X_2 the acetoclastic methanogenic bacteria and P represents the product, i.e. the methane gas. We remark that X_1 , X_2 are auto-catalysts. The reaction rates are φ_i , i = 1, 2. In the model (2), X_1 , S_1, X_2, S_2 , and P represent the concentrations of the similar components (in [g/l]). The state vector of (2) is $\boldsymbol{\xi} = \begin{bmatrix} X_1 & S_1 & X_2 & S_2 & P \end{bmatrix}^T =$ = $\begin{bmatrix} \xi_1 & \xi_2 & \xi_3 & \xi_4 & \xi_5 \end{bmatrix}^T$. The vector of feed-rates and of rates of removal of components (in gaseous form) can be written as $F = \begin{bmatrix} 0 & DS_{in} & 0 & 0 & -Q \end{bmatrix}^T$. In (2), D is the dilution rate, S_{in} represents the concentration of the externally influent substrate - glucose and Qis the methane gas outflow rate. The dynamical model (2) can be compactly written as

$$\frac{d\xi}{dt} = K \cdot \varphi(\xi) - D \cdot \xi + F \tag{3}$$

This model describes in fact the behaviour of an entire class of bioprocesses and is referred as the general dynamical state-space model of this class of bioprocesses [1]. In (3), K is the normalized matrix of the yield coefficients. The vector of reaction rates (the reaction kinetics) is

$$\varphi(\xi) = \left[\varphi_1(\xi) \ \varphi_2(\xi)\right]^T \tag{4}$$

The most difficult task for the construction of the dynamical model (3) is the modelling of the reaction kinetics (4). The form of kinetics is complex, nonlinear and in many cases unknown. A general assumption is that a reaction can take place only if all reactants are presented in the bioreactor. Therefore, the reaction rates are necessarily zero whenever the concentration of one of the reactants is zero. Thus, the reaction rates can be expressed as:

$$\varphi(\xi) = H(\xi) \cdot \alpha(\xi, t) \tag{5}$$

where $\alpha(\xi, t) = [\alpha_1(\xi, t) \alpha_2(\xi, t)]^T$ is a vector of time varying parameters. Each $\alpha_i(\xi, t), i = 1, 2$ is called the specific reaction rate. $H(\xi)$ is a 2×2 state dependent diagonal matrix, whose elements correspond to the reactions' reactants:

$$H(\xi) = \begin{bmatrix} S_1 X_1 & 0\\ 0 & S_2 X_2 \end{bmatrix}$$
(6)

 X_1 and X_2 appear because they are auto-catalysts. Then the model (3) becomes:

$$\frac{d\xi}{dt} = K \cdot H(\xi) \cdot \alpha(\xi, t) - D \cdot \xi + F$$
(7)

Another formulation for the reaction rates implies the following structure:

$$\varphi(\xi) = \left[\mu_1(\xi) \cdot X_1 \ \mu_2(\xi) \cdot X_2\right]^T \tag{8}$$

with $\mu_1(\xi)$, $\mu_2(\xi)$ the specific growth rates.

Now we can reconsider the form of the matrix $H(\xi)$ and we have:

$$H(\xi) = \begin{bmatrix} X_1 & 0\\ 0 & X_2 \end{bmatrix}$$
(9)

The model of the bioprocess can be written as:

$$\frac{d\xi}{dt} = K \cdot H(\xi) \cdot \mu(\xi, t) - D \cdot \xi + F$$
(10)

with $\mu(\xi, t) = [\mu_1(\xi, t) \mu_2(\xi, t)]^T$. For the specific growth rates $\mu(\xi, t)$ it exist many possible models, like Monod's law or Haldane kinetic model. In practice, the analytical models of the specific reaction rates $\alpha(t)$ and/or of the specific growth rates $\mu(t)$ are difficult to obtain.

3. ADAPTIVE CONTROL LAW DESIGN USING A REDUCED ORDER INPUT-OUTPUT MODEL

The major control problem for a CSTB consists the stabilization of the operational in equilibrium points [2] (the nonlinear systems can have several equilibrium points, stable or unstable). The accumulation of the acetate in the CSTB, which is an intermediate metabolite responsible for bio-methanation inhibition, is a classical symptom of the destabilization of the depollution process. The control target for the biodegradation process (3) is to regulate the acetate concentration S_2 , which is also a measure of the pollution level. The goal is then to regulate S_2 at a constant low level set point $y^* = S_2^*$ with D (the dilution rate) as control action.

The control goal can be achieved using the adaptive control, which consists in an exactly linearizing control law and an adaptation law for the unknown parameters of the bioprocess. The exactly linearizing control law can be designed using a reduced order input-output model of the process or using the complete model. In this section, the first strategy is developed. The design procedure is based on the partition of the vector of state variables in slow and fast variables, such that the singular perturbation theory can be applied [6] and subsequently a reduced order model is obtained. We suppose that the state vector of the system (2) or equivalent (3) can be partitioned as follows:

$$\xi_{S} = \begin{bmatrix} X_{1} \ S_{2} \ X_{2} \end{bmatrix}^{T}; \ \xi_{F} = \begin{bmatrix} S_{1} \ P_{1} \end{bmatrix}^{T}$$
(11)

where ξ_S represents the slow state variables and ξ_F the fast ones. This partition induces on *K* and *F* the next partitions:

$$K_{S} = \begin{bmatrix} 1 & 0 \\ k_{2} & -k_{3} \\ 0 & 1 \end{bmatrix}; \quad K_{F} = \begin{bmatrix} -k_{1} & 0 \\ 0 & k_{4} \end{bmatrix};$$
$$F_{S} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}; \quad F_{F} = \begin{bmatrix} DS_{in} \\ -Q \end{bmatrix}$$

Then, using the singular perturbation theory, the dynamic model (3) is reduced to a submodel that contains differential equations and a submodel with algebraic equations:

$$\begin{cases} \dot{\xi}_{S} = K_{S} \varphi(\xi) - D\xi_{S} + F_{S} \\ 0 = K_{F} \varphi(\xi) + F_{F} \end{cases}$$
(12)

The output of the system is the acetate concentration, which can be written as a combination of slow states:

$$y = \begin{bmatrix} 0 & 1 & 0 \end{bmatrix} \cdot \begin{bmatrix} X_1 \\ S_2 \\ X_2 \end{bmatrix} = c_S^T \cdot \xi_S$$
(13)

From equations (12), (13) we can obtain the reduced order input-output model of system (3):

$$\frac{dy}{dt} = -D \cdot y + c_S^T \cdot J \cdot F \tag{14}$$

where $J = \begin{bmatrix} I_3 & -K_S \cdot K_F^{-1} \end{bmatrix}$. The matrix K_F has full rank, so after some straightforward calculations we obtain:

_

$$J = \begin{bmatrix} 1 & 0 & 0 & \frac{1}{k_1} & 0 \\ 0 & 1 & 0 & \frac{k_2}{k_1} & \frac{k_3}{k_4} \\ 0 & 0 & 1 & 0 & -\frac{1}{k_4} \end{bmatrix}$$
(15)

The control input is the dilution rate D; therefore the vector F can be written as:

$$F = \begin{bmatrix} 0\\0\\0\\S_{in}\\0 \end{bmatrix} \cdot D + \begin{bmatrix} 0\\0\\0\\-Q \end{bmatrix}^{\Delta} = b \cdot u + \widetilde{Q}$$
(16)

Then the reduced order input-output model (14) becomes

$$\frac{dy}{dt} = -D \cdot y + c_S^T J b \cdot D + c_S^T J \widetilde{Q}$$
(17)
where $c_S^T J b = \frac{k_2}{k_1} S_{in}$ and $c_S^T j \widetilde{Q} = -\frac{k_3}{k_4} Q$.

The exactly linearizing control law for the process (3) is obtained in three steps (for general point of view see Isidori [5], Bastin and Dochain [1]. First one obtains after straightforward calculations an input-output model for the process. In this section we use the reduced order input-output model (17). Second we consider a stable linear reference model for tracking error $y^* - y = S_2^* - S_2$, where $y^* = S_2^*$ is the desired output trajectory (the set point).

$$\frac{d}{dt}\left(y^* - y\right) + \lambda\left(y^* - y\right) = 0, \ \lambda > 0 \tag{18}$$

Finally, the exactly linearizing feedback control law is obtained by calculus of u(t) = D(t) such that the input-output model has the same behaviour with the reference model. The control law is obtained by substituting (17) into (18):

$$u(t) = D(t) = \frac{1}{\frac{k_2}{k_1} S_{in} - y} \left(\frac{dy^*}{dt} + \lambda (y^* - y) + \frac{k_3}{k_4} Q \right) \quad (19)$$

The exactly linearizing control law is obtained with the assumption that the functional form of the nonlinearities as well as the process parameters are known. Such prior knowledge is not realistic, in fact the bioprocess parameters are imprecisely known, or, still worse, completely unknown. The control law (19) has the advantage that it not depends on the kinetics of the process. However, if one or more of the yield coefficients are unknown, it is necessary to design an adaptation law for these coefficients. For example, if the ratio $\theta = k_2 / k_1$ is unknown or uncertain, the adaptation law, obtainable by means of a Lyapunov technique, is of the form:

$$\frac{d\hat{\theta}}{dt} = \gamma DS_{in} \left(y^* - y \right), \ \gamma > 0$$
⁽²⁰⁾

where $\hat{\theta}$ is the on-line estimate of the unknown parameter θ . Then the adaptive linearizing control law is obtained from (19) and (20):

$$\begin{cases} \frac{d\hat{\Theta}}{dt} = \gamma DS_{in} \left(y^* - y \right), \quad \gamma > 0\\ u(t) = \frac{1}{\hat{\Theta}S_{in} - y} \left(\dot{y}^* + \lambda \left(y^* - y \right) + \left(k_3 / k_4 \right) Q \right)^{(21)} \end{cases}$$

The design procedure based on the reduced order input-output model provides good results only if the partition of the state vector in slow and fast variables is in accordance with the reality of the physical process. If not, this partition cannot be done and the singular perturbations theory cannot be applied. Therefore, the reduced order model cannot be obtained and it is necessary to use the complete input-output model of the bioprocess in order to design the exactly linearizing control law.

4. ADAPTIVE CONTROL LAW DESIGN USING THE COMPLETE MODEL OF THE BIOPROCESS

4.1. Exactly linearizing control law design

The control goal is the same as in Section 3. The design procedure for exactly linearizing control law comprises the classical three steps as in previous section, but the complete model of the bioprocess is used. First one obtains from (2) the input-output model of the process, with $y = S_2$ and u = D:

$$\frac{dy}{dt} = k_2 \varphi_1(\xi) - k_3 \varphi(\xi) - u \cdot y \tag{22}$$

It can be noticed that the reaction kinetics must be modelled or estimated. We suppose that the reaction rates are of the form (8). Then the input-output model (22) can be written as

$$\frac{dy}{dt} = k_2 \mu_1(S_1) X_1 - k_3 \mu_2(y) X_2 - u \cdot y$$
(23)

We consider that the specific growth rates are:

$$\mu_1(S_1) = \mu_1^* \frac{S_1}{K_{M_1} + S_1}$$
(24)

$$\mu_2(y) = \mu_2(S_2) = \mu_2^0 \frac{S_2}{K_{M_2} + S_2 + S_2^2 / K_i}$$
(25)

with $\mu_2^0 = \mu_2^*(1 + \sqrt{K_{M_2}/K_i})$. The first specific growth rate (24) is the Monod law and the specific growth rate (25) is the Haldane kinetic model that takes into account the substrate inhibition on the growth. K_{M_1}, K_{M_2} are Michaelis-Menten constants; μ_1^*, μ_2^* represent the maxim specific growth rates and K_i is the inhibition constant.

In the second step of the design procedure, we impose a desired trajectory for the process output, such that we have a first order linear stable closed loop (process plus controller) dynamical behaviour of the form (18):

$$\frac{d}{dt}\left(y^* - y\right) + \lambda\left(y^* - y\right) = 0, \ \lambda > 0$$
(26)

Finally, in the third step, the exactly linearizing feedback control law is obtained by calculus of u(t) = D(t) such that the input-output model has the same behaviour with the reference model. The control law is obtained by substituting (23) into (26):

$$u(t) = \frac{1}{y} \Big[k_2 \mu_1(S_1) X_1 - k_3 \mu_2(y) X_2 - \dot{y}^* - \lambda \Big(y^* - y \Big) \Big]$$
(27)

The implementation of exactly linearizing control law (27) (also the laws (19) or (21)) must to take into consideration the preservation of the denominator away from zero.

The exactly linearizing control law is obtained with the assumption that reaction kinetics $\varphi(\xi)$ is known. Such prior knowledge is not realistic, in fact in practice the specific growth rates (24), (25) are imprecisely known or completely unknown. Another problem is the uncertainty of the yield coefficients. Therefore it is necessary to design on-line estimation strategies for the specific growth rates and/or adaptation laws for unknown coefficients. The the exactly linearizing control law (27) will be combined with these estimators and finally we can obtain the adaptive linearizing control law for the biomethanation process.

4.2. Adaptation law design

First, we provide an example of adaptation law design for an unknown yield coefficient. We consider that the yield coefficient k_3 is unknown, but the prior information about the ratio $k = k_2/k_3$ is available. The design procedure of the adaptation law for the unknown

parameter $\theta = k_3$ can be completed using a Lyapunov technique. The input-output model (23) can be parameterized in the form:

$$\frac{dy}{dt} = \theta [k\mu_1(S_1)X_1 - \mu_2(y)X_2] - u \cdot y$$
(28)

Considering the previous parameterization, the adaptation law for $\theta = k_3$ is:

$$\frac{d\hat{\theta}}{dt} = \eta(\xi, y) \tag{29}$$

where $\hat{\theta}$ is an on-line estimate of the unknown (but constant) parameter $\theta = k_3$. The adaptive version of the linearizing control law (27) consists of replacing the unknown parameter by the on-line estimate calculated with the adaptation mechanism (29):

$$u(t) = \frac{1}{y} \left(\hat{\theta} [k\mu_1(S_1)X_1 - \mu_2(y)X_2] - \dot{y}^* - \lambda (y^* - y) \right) \quad (30)$$

The design is based on the choice of the adaptation law $\eta(\xi, y)$ such that the closed loop system is stable. Let δ be a known positive scalar. Consider the Lyapunov function given by:

$$V(t) = \frac{1}{2} \left(\left(y^* - y \right)^2 + \delta^{-1} \left(\theta - \hat{\theta} \right)^2 \right)$$
(31)

The time derivative of Lyapunov function (31) along the trajectories of the system (28) is obtained, after use of (29), (30) and after some manipulations, as:

$$\frac{dV}{dt} = -\lambda (y^* - y)^2 - (\theta - \hat{\theta})^2 \cdot (\delta^{-1} \eta(\xi, y) + (k\mu_1(S_1)X_1 - \mu_2(y)X_2)(y^* - y)]$$
(32)

Choosing the adaptation law by the form:

$$\eta(\xi, y) = -\delta(k\mu_1(S_1)X_1 - \mu_2(y)X_2)(y^* - y) \quad (33)$$

one obtains: $\dot{V}(t) = -\lambda (y^* - y)^2 \le 0$ and is clear that the Lyapunov function decreases along the trajectories of the controlled system.

Finally, the nonlinear adaptive controller consists of the linearizing control law (30) and of the direct adaptation law (29), (33):

$$\begin{cases} \frac{d\hat{\theta}}{dt} = -\delta(k\mu_1(S_1)X_1 - \mu_2(y)X_2)(y^* - y) \\ u(t) = \frac{1}{y} \left(\hat{\theta}[k\mu_1(S_1)X_1 - \mu_2(y)X_2] - \dot{y}^* - \lambda(y^* - y) \right) \end{cases}$$
(34)

4.3. High gain observer for reaction kinetics

For on-line estimation of the specific growth rates $\mu(t)$ an algorithm based on high-gain technique can be designed [11]. The model (10) can be rewritten as:

$$\frac{d\xi}{dt} = K \cdot H(\xi) \cdot \rho(t) - D \cdot \xi + F$$
(35)

where $\rho(t) = \mu(t)$ is the vector of unknown specific growth rates and $H(\xi)$ is of the form (9). The design of a high gain observer for the system (35) implies a factorization of the yield matrix K. This factorization is possible only if the matrix is of full rank, which is true for our particular model, and for general case is a generic property. Moreover, we shall suppose that all state variables are measured (contrarily, a state estimator can be used). Another hypothesis regards the boundedness of the kinetics, which is in accordance with practice. The design of nonlinear high gain observers is done in [3] with assumptions about the boundedness of $H(\xi)$ diagonal elements' away from zero.

We choose the next factorization of yield matrix *K* of the biomethanation process:

$$K_{a} = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}; \quad K_{b} = \begin{bmatrix} -k_{1} & 0 \\ k_{2} & -k_{3} \\ 0 & -k_{4} \end{bmatrix}$$
(36)

and consequently we obtain:

$$\xi_{a} = \begin{bmatrix} X_{1} & X_{2} \end{bmatrix}^{T}; \xi_{b} = \sigma = \begin{bmatrix} S_{1} & S_{2} & P \end{bmatrix}^{T};$$

$$F_{a} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}; F_{b} = \begin{bmatrix} D \cdot S_{in} \\ 0 \\ -Q \end{bmatrix}$$
(37)

It is clear that K_a is full rank matrix. For this factorization of yield matrix K is possible to design an observer for on-line estimation of the specific growth rates $\rho(t) = \mu(t)$. The high gain based observer equations for a general bioprocess described by the model (35) are [3]:

$$\hat{\xi}_a = K_a H(\hat{\xi}_a, \xi_b)\hat{\rho} - D\hat{\xi}_a + F_a - 2\beta(\hat{\xi}_a - \xi_a)$$
(38)

$$\dot{\hat{\rho}} = -\beta^2 \cdot \left[K_a \cdot H(\hat{\xi}_a, \xi_b) \right]^{-1} \cdot (\hat{\xi}_a - \xi_a)$$
(39)

The estimator (38), (39) is in fact a copy of the bioprocess model, but with state ξ_a replaced by its estimate $\hat{\xi}_a$, and with a corrective term. The tuning of this observer is very simple because a

single parameter is involved: β . The high gain estimator (38), (39) can be applied for the biomethanation process considering the matrix $H(\xi)$ of the form (9) and the factorization (36), (37). The equations of the observer are [11]:

$$\frac{d}{dt} \begin{bmatrix} \hat{X}_1 \\ \hat{X}_2 \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} \hat{X}_1 & 0 \\ 0 & \hat{X}_2 \end{bmatrix} \begin{bmatrix} \hat{\mu}_1 \\ \hat{\mu}_2 \end{bmatrix} - D \begin{bmatrix} \hat{X}_1 \\ \hat{X}_2 \end{bmatrix} - 2\beta \begin{bmatrix} \hat{X}_1 - X_1 \\ \hat{X}_2 - X_2 \end{bmatrix}$$
(40)
$$\frac{d}{dt} \begin{bmatrix} \hat{\mu}_1 \\ \hat{\mu}_2 \end{bmatrix} = -\beta^2 \cdot \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \cdot \begin{bmatrix} \hat{X}_1 & 0 \\ 0 & \hat{X}_2 \end{bmatrix} \end{bmatrix}^{-1} \cdot \begin{bmatrix} \hat{X}_1 - X_1 \\ \hat{X}_2 - X_2 \end{bmatrix}$$
(41)

The final adaptive control law designed using the complete input-output model of the biodegradation process comprises the exactly linearizing control law (27), the adaptation law (29), (33) and the high gain estimator (40), (41):

$$\begin{cases} \frac{d}{dt} \begin{bmatrix} \hat{X}_1 \\ \hat{X}_2 \end{bmatrix} = K_a \begin{bmatrix} \hat{X}_1 & 0 \\ 0 & \hat{X}_2 \end{bmatrix} \begin{bmatrix} \hat{\mu}_1 \\ \hat{\mu}_2 \end{bmatrix} - D \begin{bmatrix} \hat{X}_1 \\ \hat{X}_2 \end{bmatrix} - 2\beta \begin{bmatrix} \hat{X}_1 - X_1 \\ \hat{X}_2 - X_2 \end{bmatrix} \\ \frac{d}{dt} \begin{bmatrix} \hat{\mu}_1 \\ \hat{\mu}_2 \end{bmatrix} = -\beta^2 \cdot \left[\begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \cdot \begin{bmatrix} \hat{X}_1 & 0 \\ 0 & \hat{X}_2 \end{bmatrix} \right]^{-1} \cdot \begin{bmatrix} \hat{X}_1 - X_1 \\ \hat{X}_2 - X_2 \end{bmatrix} \\ \frac{d\hat{\theta}}{dt} = -\delta (k\hat{\mu}_1 X_1 - \hat{\mu}_2 X_2) (y^* - y) \\ u(t) = \frac{1}{y} (\hat{\theta} \cdot [k\hat{\mu}_1 X_1 - \hat{\mu}_2 X_2] - \dot{y}^* - \lambda (y^* - y)) \end{cases}$$
(42)

The block scheme of the controlled bioprocess is presented in Fig. 1.



Fig. 1. The scheme of the controlled bioprocess

Remark: The "estimates" \hat{X}_1 , \hat{X}_2 used in the high gain algorithm are in fact outputs of a kind of state observer and they are compared with the real measurements of X_1 , X_2 in order to estimate

the specific growth rates. It can be seen also that only the measurements of y, X_1 and X_2 are needed for the control input design.

4.4. Simulation results

The simulated control tasks were performed for the following bioreactor parameters:

$$\begin{split} S_{in} &= 15g \, / \, l; \, k_1 = 5.4; \, k_2 = 10; \, k_3 = 14.7; \\ k_4 &= 80; \, Q = 0; \, \mu_1^* = 0.6h^{-1}; \, \mu_2^0 = 0.8h^{-1}; \\ K_{M_1} &= 0.75g \, / \, l; \, K_{M_2} = 1g \, / \, l; \, K_i = 21g \, / \, l \end{split}$$

Three simulation cases were considered in order to test the performances of the proposed control laws.

Case 1. The exactly linearizing controller (27) (for $\lambda = 1$) was implemented for the bioprocess, in order to stabilize the output $y = S_2$ to the reference value $y^* = S_2^* = 5g/l$. All yield coefficients and the specific growth rates are supposed known (the relations (24), (25) were used). The performances of the controlled process are depicted in Fig. 2, where the output (the acetate concentration) and the set point (the constant desired output trajectory) are shown. Fig. 3 portrays the control input signal u(t).

Case 2. In this simulation case, the parameter $\theta = k_3$ and the specific growth rates μ_1, μ_2 are regarded as unknown. The control task was the stabilization of the output to the same constant value as in the case 1. This goal is accomplished using the adaptive linearizing controller (42) (the scheme from Fig. 1), with the controller parameters $\lambda = 1, \delta = 20, \beta = 3$. Evolution of the output is presented in Fig. 4 and the control action for the adaptive controller is depicted in Fig. 5. The on-line estimate $\hat{\theta}$ of unknown parameter is presented in Fig. 6. Fig. 7 and 8 portray the evolution of the on-line estimated specific growth rates versus their true values. However, while the prior information is less than in the exactly case, it can be observed that the resulting responses are good.













Fig. 6. Evolution of the estimated parameter θ









Fig. 9. Time profile of the output (noisy data -case 3)

The level of the acetate concentration is low; therefore the level of pollution is low.

Case 3. The performances of the proposed adaptive controller are analysed also for noisy data of X_1 , X_2 , and the obtained results are quite good.

The simulation conditions and the tuning parameters are the same as in the case 2.

The measurements of X_1 and X_2 are vitiated by an additive Gaussian noise. This noise is with zero mean and amplitude equal to 4% of the free-noise values. Fig. 9 depicts the output evolution in this last case and Fig. 10 portrays the time profile of the estimated specific growth rate μ_1 .



Fig. 10. Estimates of μ_1 (case 3: noisy data of X_1, X_2)

Notice that the values of the tuning parameters of the adaptation law and of the high gain estimator are chosen such that a compromise between a good estimation and noise rejection is establish.

5. CONCLUSIONS

In this work nonlinear adaptive controllers were designed for a biodegradation process that takes place inside a CSTB. The adaptive design is based on input-output models of the bioprocess (reduced order or complete models). An adaptation law for an unknown yield parameter is obtained by means of Lyapunov functionbased strategy. This adaptation law for the parameter estimation error is of direct type. Furthermore, the unknown specific growth rates are estimated using a high gain observer. The adaptive controller for the bioprocess consists in the exactly linearizing control law, the adaptation mechanism for the unknown yield parameter and the high gain estimator. The simulation results show the good behaviour of the adaptive controller, which use minimal information from the process. Good performances are obtained also in the case of noisy measurements of the state variables.

ACKNOWLEDGMENT

This work was supported by the CNCSIS, grant no. 33062/317, 2004.

REFERENCES

- [1] Bastin, G., Dochain, D., *On-line Estimation* and Adaptive Control of Bioreactors, Elsevier, 1990.
- [2] Bastin, G., Nonlinear and adaptive control in biotechnology: a tutorial, *European Control Conference ECC'91*, Grenoble, 1991, pp. 2001–2012.
- [3] Farza, M., Busawon, K., Hammouri, H., Simple Nonlinear Observers for On-line Estimation of Kinetic Rates in Bioreactors. *Automatica*, vol. 34, no. 3, pp. 301 – 318, 1998.
- [4] Gauthier, J.P., Hammouri, H., Othman, S., A Simple Observer for Nonlinear Systems. Applications to Bioreactors. *IEEE Transactions in Automatic Control*, vol. 37, no. 6, pp. 875 – 880, 1992.
- [5] Isidori, A., *Nonlinear control Systems*. Springer Verlag, 1989.
- [6] Kokotovic, P.V., Khalil, H.K., O'Reilly, J., Singular Perturbations Method in Control: Analysis and Design. Academic Press, London, 1986.
- [7] Narendra, K.S., Ortega, R., Dorato, P., *Advances in adaptive control.* IEEE Press: Piscataway, N.J., 1991.
- [8] Nielsen, M.K., Madsen, H., Carstensen, J., Processes in wastewater treatment plants. *The 3rd IEEE Conf. on Ctr.App.*, Glasgow, 1994, pp.1005-1010.
- [9] Sastry, S., Isidori, A., Adaptive control of linearizable systems. *IEEE Tr. on Autom. Contr.*, AC-35, no. 9, pp. 1123-1131, 1989.
- [10] Selişteanu, D., Petre, E., Ionete, C., High Gain Observers for Estimation of Kinetics in a Bioreactor. *Annals of the University of Craiova, Electrical Engineering Series*, vol. 21, pp. 378 – 388, 1997.
- [11] Selişteanu, D., Petre, E., Şendrescu, D., Modelling and Identification of Wastewater Biodegradation Process. *The 12th International Symposium SIMSIS 12*, Galaţi, 2004, pp. 149-154.